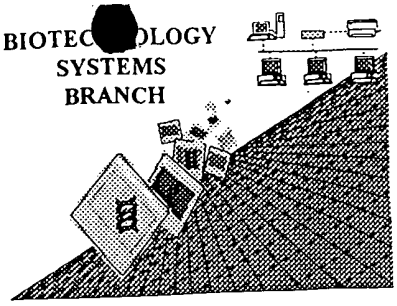
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/840,243

Source: OIPE

Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/840,243

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

11 ____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001
TIME: 17:52:54

Input Set : A:\SEQ LIST 010830-117
Output Set: N:\CRF3\05072001\I840243.raw

```
     3 <110> APPLICANT: NOVIMMUNE SA c/o MEDABIOTECH SA
     5 <120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
     6       SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION
     7       FACTOR AND MEDICAL USES OF THESE SUBSTANCES
     9 <130> FILE REFERENCE: B3991A-GD/LL
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/840,243
C--> 12 <141> CURRENT FILING DATE: 2001-04-24
    14 <150> PRIOR APPLICATION NUMBER: 98120085.0
    15 <151> PRIOR FILING DATE: 1998-10-24
    17 <160> NUMBER OF SEQ ID NOS: 19
    19 <170> SOFTWARE: PatentIn Ver. 2.1
```

Does Not Comply
Corrected Diskette Needed
pp. 1-2

ERRORED SEQUENCES

```
   431 <210> SEQ ID NO: 15
   432 <211> LENGTH: (37)
   433 <212> TYPE: PRT
   434 <213> ORGANISM: Homo sapiens
   436 <400> SEQUENCE: 15
   437 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
   438   1               5                  10                  15
   440 Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
   441             20                  25                  30
   443 Ala Ala Gly Ala
E--> 444         35 (36)
   475 <210> SEQ ID NO: 18
   476 <211> LENGTH: 220
   477 <212> TYPE: PRT
   478 <213> ORGANISM: Homo sapiens
   480 <400> SEQUENCE: 18
   481 Asn Ala Phe Asn Val Phe Thr Phe Val Phe His Leu Ala Glu Cys Asn
   482   1               5                  10                  15
E--> 484 Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val(Xaa)Thr
   485             20                  25                  30
   487 Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
   488         35                  40                  45
   490 Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
   491     50                  55                  60
   493 Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
   494 65                  70                  75                  80
   496 Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
   497                 85                  90                  95
   499 Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
   500             100                 105                 110
   502 Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
   503         115                 120                 125
```

Number of amino acids differ:
- 37 listed
- 36 shown

Missing mandatory <220> to <223> features to explain the "Xaa's" in the sequence. See #10 on the Error Summary sheet.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001
TIME: 17:52:54

Input Set : A:\SEQ LIST 010830-117
Output Set: N:\CRF3\05072001\I840243.raw

```
     505 Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
     506     130                 135                 140
E--> 508 Asp Ile Val Xaa Met Leu Leu Asp Cys Gly Val Asp Val Asn Xaa Tyr
     509 145                 150                 155                 160
     511 Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
     512                 165                 170                 175
     514 Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
     515             180                 185                 190
     517 Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
     518         195                 200                 205
     520 Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
     521     210                 215                 220
```

See p. 1

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001
TIME: 17:52:55

Input Set : A:\SEQ LIST 010830-117
Output Set: N:\CRF3\05072001\I840243.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:444 M:252 E: No. of Seq. differs, <211>LENGTH:Input:37 Found:36 SEQ:15
L:484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
M:340 Repeated in SeqNo=18